```
RESULT 2
A29947
prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - sheep
N;Alternate names: prostaglandin endoperoxide synthetase
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29947
R;Merlie, J.P.; Fagan, D.; Mudd, J.; Needleman, P.
J. Biol. Chem. 263, 3550-3553, 1988
A;Title: Isolation and characterization of the complementary DNA for sheep seminal ves
A;Reference number: A29947; MUID:88153641; PMID:2831188
A;Accession: A29947
A;Molecule type: mRNA
A;Residues: 1-599
A;Cross-references: UNIPROT:P05979; UNIPARC:UPI000016C5E8; GB:M18243; NID:g165843; PID
C;Superfamily: human prostaglandin-endoperoxide synthase; EGF homology
C;Keywords: oxidoreductase
F;1-23/Domain: signal sequence #status predicted
F;24-599/Product: prostaglandin-endoperoxide synthase #status predicted
F;35-68/Domain: EGF homology

  Query Match             85.9%;  Score 2956.5;  DB 2;  Length 599;
  Best Local Similarity   90.6%;  Pred. No. 2.4e-227;
  Matches  539;  Conservative   24;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          39 RWPLLLLLLLLLPPPPVLPAEARTPAPVNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYS 98
               |:|   |||||| | ||  |:   ||||||||||||||||||||||||||||||||||||
Db           8 RFP---LLLLLLSPSPVFSADPGAPAPVNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYS 64

Qy          99 GPNCTIPELWTWLRNSLRPSPSFLHFLLTHGRWFWEFINATFIRDMLMRLVLTARSNLIP 158
               ||||||||:||||| :|||||||:||||||||| |:|:||||||| ||||||| ||||||
Db          65 GPNCTIPEIWTWLRTTLRPSPSFIHFLLTHGRWLWDFVNATFIRDTLMRLVLTVRSNLIP 124

Qy         159 SPPTYNIAHDYISWESFSNVSYYTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRR 218
               |||||||||||||||||||||||||:|||||:|||||||||||||||||: | |||||||
Db         125 SPPTYNIAHDYISWESFSNVSYYTRILPSVPRDCPTPMGTKGKKQLPDAEFLSRRFLLRR 184

Qy         219 KFIPDPQGTNLMFAFFAQHFTHQFFKTSGKMGPGFTKALGHGVDLGHIYGDNLDRQYQLR 278
               |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db         185 KFIPDPQGTNLMFAFFAQHFTHQFFKTSGKMGPGFTKALGHGVDLGHIYGDNLERQYQLR 244

Qy         279 LFKDGKLKYQVLDGEMYPPSVEEAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLW 338
               ||||||||||:|:||:|||||||||||||||||| |||||||||||||||||||||||:|
Db         245 LFKDGKLKYQMLNGEVYPPSVEEAPVLMHYPRGIPPQSQMAVGQEVFGLLPGLMLYATIW 304

Qy         339 LREHNRVCDLLKAEHPTWGDEQLFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPEL 398
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         305 LREHNRVCDLLKAEHPTWGDEQLFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPEL 364

Qy         399 LFSAQFQYRNRIAMEFNQLYHWHPLMPDSFWVGSQEYSYEQFLFNTSMLTHYGIEALVDA 458
               || ||||||||||||||||||||||||||| || |:|||||||||||||  ||:||||||
Db         365 LFGAQFQYRNRIAMEFNQLYHWHPLMPDSFRVGPQDYSYEQFLFNTSMLVDYGVEALVDA 424

Qy         459 FSRQSAGRIGGGRNIDHHVLHVAVETIKESRELRLQPFNEYRKRFGMRPYMSFQELTGEK 518
               |||| |||||||||||||:|||||: ||||| |||||||||||||||:|| |||||||||
Db         425 FSRQPAGRIGGGRNIDHHILHVAVDVIKESRVLRLQPFNEYRKRFGMKPYTSFQELTGEK 484

Qy         519 EMAAELEELYGDIDALEFYPGLLLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYW 578
               |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db         485 EMAAELEELYGDIDALEFYPGLLLEKCHPNSIFGESMIEMGAPFSLKGLLGNPICSPEYW 544
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Qy          579 KPSTFGGEMGFNMVKTATLKKLVCLNTKTCPYVSFRVPDPHQDGGPGVERPSTEL 633
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Db          545 KASTFGGEVGFNLVKTATLKKLVCLNTKTCPYVSFHVPDPRQEDRPGVERPPTEL 599
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RESULT 8
AX082872
LOCUS       AX082872                2587 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 1 from Patent WO0111026.
ACCESSION   AX082872
VERSION     AX082872.1  GI:13184804
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1
  AUTHORS   Gierse,J.K.
  TITLE     Canine cyclooxygenase-1 (cox-1) and cyclooxygenase-2 (cox-2)
  JOURNAL   Patent: WO 0111026-A 1 15-FEB-2001;
            G.D. SEARLE & CO. (US)
FEATURES             Location/Qualifiers
     source          1..2587
                     /organism="Canis familiaris"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9615"
ORIGIN

  Query Match             96.5%;  Score 265.4;  DB 2;  Length 2587;
  Best Local Similarity   97.8%;  Pred. No. 1.9e-77;
  Matches  269;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 TTTGCACAACACTTCACCCACCAGTTCTTCAAAACTTCTGGCAAGATGGGTCCTGGCTTC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        623 TTTGCACAACACTTCACCCATCAGTTCTTCAAAACTTCTGGCAAGATGGGTCCTGGCTTC 682

Qy         61 ACCAAGGCCTTGGGCCATGGGGTAGATCTTGGTCACATTTATGGGGACAATCTGGACCGT 120
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        683 ACCAAGGCCTTGGGCCATGGGGTAGATCTTGGCCACATTTATGGGGACAATCTGGACCGT 742

Qy        121 CAGTATCAGCTGCGGCTCTTTAAGGATGGGAAACTCAAGTATCAGGTTCTGGATGGAGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 CAGTATCAGCTGCGGCTCTTTAAGGATGGGAAACTCAAGTATCAGGTTCTGGATGGAGAG 802

Qy        181 ATGTACCCGTCATCTGTGGAGGAGGCGCCTGTGTTGATGCACTACCCACGGGGCATTCTG 240
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 ATGTACCCGCCATCTGTGGAGGAGGCGCCTGTGTTGATGCACTACCCACGGGGCATTCTG 862

Qy        241 CCCCAGAGTCAGATGGCTGTGGGCCAGGAGGTGTT 275
              ||||||||||||||||| |||||||| || |||||
Db        863 CCCCAGAGTCAGATGGCCGTGGGCCAAGAAGTGTT 897
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60/147,601
US Abandoned.

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RESULT 4
ABB07241
ID   ABB07241 standard; protein; 608 AA.
XX
AC   ABB07241;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Canine cyclooxygenase-1 (COX-1) protein.
XX
KW   Cyclooxygenase; COX-1; COX-2; canine; arthritis; cancer; neoplasia;
KW   inflammation; central nervous system; dog.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 15. .34
FT                   /note= "residues Xaa are unknown; the encoding codons are
FT                   not indicated in the corresponding DNA sequence"
XX
PN   WO200111026-A1.
XX
PD   15-FEB-2001.
XX
PF   04-AUG-2000; 2000WO-US019565.
XX
PR   06-AUG-1999;   99US-0147601P.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Gierse JK;
XX
DR   WPI; 2002-113777/15.
DR   N-PSDB; ABA94341.
XX
PT   Novel substantially purified canine cyclooxygenase 1 or 2 protein, useful
PT   for identifying drugs that can reduce inflammation in dogs, and screening
PT   selective inhibitors of cyclooxygenase-2 protein.
XX
PS   Claim 11; Page 81-83; 122pp; English.
XX
CC   The invention relates to genes that encode canine cyclooxygenase (COX)-1
CC   or COX-2 proteins. The COX proteins, especially COX-2 is useful for
CC   diagnosing or prognosing a COX-2 related condition in a dog. COX-2 or its
CC   fragment is useful for identifying a test material which has the ability
CC   to inhibit, suppress, modulate, or maintain canine COX-2 activity. The
CC   COX-1 and COX-2 polynucleotides are useful for determining an association
CC   between a polymorphism and a trait. COX-2 cDNA molecules and methods
CC   provided are also useful for diagnosing or prognosing COX-2 related
CC   condition such as arthritis, cancer, neoplasia, inflammation or central
CC   nervous system disorder in a dog. The present sequence represents a
CC   canine COX-1 protein
XX
SQ   Sequence 608 AA;

  Query Match             90.7%;  Score 574;  DB 5;  Length 608;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  574;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         60 ARTPAPVNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYSGPNCTIPELWTWLRNSLRPSP 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 ARTPAPVNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYSGPNCTIPELWTWLRNSLRPSP 94

Qy        120 SFLHFLLTHGRWFWEFINATFIRDMLMRLVLTARSNLIPSPPTYNIAHDYISWESFSNVS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 SFLHFLLTHGRWFWEFINATFIRDMLMRLVLTARSNLIPSPPTYNIAHDYISWESFSNVS 154

Qy        180 YYTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRRKFIPDPQGTNLMFAFFAQHFT 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 YYTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRRKFIPDPQGTNLMFAFFAQHFT 214

Qy        240 HQFFKTSGKMGPGFTKALGHGVDLGHIYGDNLDRQYQLRLFKDGKLKYQVLDGEMYPPSV 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 HQFFKTSGKMGPGFTKALGHGVDLGHIYGDNLDRQYQLRLFKDGKLKYQVLDGEMYPPSV 274

Qy        300 EEAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLWLREHNRVCDLLKAEHPTWGDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 EEAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLWLREHNRVCDLLKAEHPTWGDE 334

Qy        360 QLFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFSAQFQYRNRIAMEFNQLYH 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 QLFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFSAQFQYRNRIAMEFNQLYH 394

Qy        420 WHPLMPDSFWVGSQEYSYEQFLFNTSMLTHYGIEALVDAFSRQSAGRIGGGRNIDHHVLH 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 WHPLMPDSFWVGSQEYSYEQFLFNTSMLTHYGIEALVDAFSRQSAGRIGGGRNIDHHVLH 454

Qy        480 VAVETIKESRELRLQPFNEYRKRFGMRPYMSFQELTGEKEMAAELEELYGDIDALEFYPG 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 VAVETIKESRELRLQPFNEYRKRFGMRPYMSFQELTGEKEMAAELEELYGDIDALEFYPG 514

Qy        540 LLLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYWKPSTFGGEMGFNMVKTATLKK 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 LLLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYWKPSTFGGEMGFNMVKTATLKK 574

Qy        600 LVCLNTKTCPYVSFRVPDPHQDGGPGVERPSTEL 633
              ||||||||||||||||||||||||||||||||||
Db        575 LVCLNTKTCPYVSFRVPDPHQDGGPGVERPSTEL 608
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Database :        GenEmbl:*
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                 2:  gb_pat:*
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                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
                 11:  gb_ov:*
                 12:  gb_htg:*
                 13:  gb_in:*
                 14:  gb_om:*
                 15:  gb_ba:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                    %
Result              Query
   No.   Score      Match  Length  DB  ID                          Description
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     1    2693      100.0    2693   2  AR411935  own               AR411935 Sequence
c    2    2693      100.0    2693   2  AR411936  own               AR411936 Sequence
     3  2677.4       99.4    2706  14   AF535138 bad date           AF535138 Canis fam
     4  2561.2       95.1    2587   2  AX082872  bad date          AX082872 Sequence
     5    1899       70.5    1899   2  AR411937                    AR411937 Sequence
c    6    1899       70.5    1899   2  AR411938                    AR411938 Sequence
     7  1799.6       66.8    2646   5  BC029840                    BC029840 Homo sapi
     8  1797.6       66.8    4286   7  BV177208                    BV177208 sqnm93421
     9  1796.6       66.7    2611  14   OAPGES                      Y00750 Sheep mRNA
    10  1794.2       66.6    2554   2  CS113056                    CS113056 Sequence
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    12  1794.2       66.6    2554   2  AX082876                    AX082876 Sequence
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    15  1791.6       66.5    2611   2  E02077                      E02077 cDNA encodi
    16  1771.2       65.8    2554   2  AR029277                    AR029277 Sequence
    17  1759.2       65.3    2666  14   SHPPGS                      J03599 Sheep prost
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RESULT 3
AF535138
LOCUS       AF535138                2706 bp    mRNA    linear   MAM 16-OCT-2002
DEFINITION  Canis familiaris cyclooxygenase mRNA, complete cds.
ACCESSION   AF535138
VERSION     AF535138.1  GI:23452498
KEYWORDS    .
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1  (bases 1 to 2706)
  AUTHORS   Chandrasekharan,N.V., Dai,H., Roos,K.L.T., Evanson,N.K., Tomsik,J.,
            Elton,T.S. and Simmons,D.L.
  TITLE     COX-3, a cyclooxygenase-1 variant inhibited by acetaminophen and
            other analgesic/antipyretic drugs: Cloning, structure, and
            expression
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (21), 13926-13931 (2002)
   PUBMED   12242329
REFERENCE   2  (bases 1 to 2706)
  AUTHORS   Chandrasekharan,N.V., Dai,H., Roos,L.T., Evanson,N.K., Tomsik,J.,
            Elton,T.S. and Simmons,D.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-AUG-2002) Chemistry and Biochemistry, Brigham Young
            University, Provo, UT 84602, USA
FEATURES             Location/Qualifiers
     source          1. .2706
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     CDS             28. .1929
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                     /db_xref="GI:23452499"
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                     LRLFKDGKLKYQVLDGEMYPPSVEEAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLY
                     ATLWLREHNRVCDLLKAEHPTWGDEQLFQTARLILIGETIKIVIEEYVQQLSGYFLQL
                     KFDPELLFSAQFQYRNRIAMEFNQLYHWHPLMPDSFWVGSQEYSYEQFLFNTSMLTHY
                     GIEALVDAFSRQSAGRIGGGRNIDHHVLHVAVETIKESRELRLQPFNEYRKRFGMRPY
                     MSFQELTGEKEMAAELEELYGDIDALEFYPGLLLEKCHPNSIFGESMIEIGAPFSLKG
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                     GVQRPSTEL"
ORIGIN

  Query Match             99.4%;  Score 2677.4;  DB 14;  Length 2706;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2681;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          7 CGAGCGCAGCAGCCGCCCAGAGCTATGAGCCGTGAGTTCGACCCTGAGGCCCCCAGGAAC 66
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Db          4 CGAGCGCAGCAGCCGCCCAGAGCTATGAGCCGTGAGTTCGACCCTGAGGCCCCCAGGAAC 63

Qy         67 CCTCTTCGCCTCCCGGGGGAGCCTCGAATGCCAGGCCCAGCCCTCACCTCTCGCTCCGCA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CCTCTTCGCCTCCCGGGGGAGCCTCGAATGCCAGGCCCAGCCCTCACCTCTCGCTCCGCA 123
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Qy        127 GGGGGGAGTCGCCTGCACCGGTGGCCGCTGCTCCTGCTGCTGCTGCTGCTGCTGCCGCCG 186
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Db        124 GGGGGGAGTCGCCTGCACCGGTGGCCGCTGCTCCTGCTGCTGCTGCTGCTGCTCCCGCCG 183

Qy        187 CCCCCGGTCCTGCCCGCGGAAGCCCGGACCCCGGCGCCTGTGAACCCGTGTTGTTACTAC 246
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Db        184 CCCCCGGTCCTGCCCGCGGAAGCCCGGACCCCGGCGCCTGTGAACCCGTGTTGTTACTAC 243

Qy        247 CCATGTCAGCACCAAGGGATCTGTGTCCGCTTCGGCCTTGACCGCTACCAGTGTGACTGC 306
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Qy        307 ACCCGCACGGGCTATTCTGGCCCCAACTGCACCATCCCCGAGCTGTGGACCTGGCTCCGG 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ACCCGCACGGGCTATTCTGGCCCCAACTGCACCATCCCCGAGCTGTGGACCTGGCTCCGG 363

Qy        367 AATTCACTGCGCCCCAGTCCCTCTTTCCTCCACTTCCTGCTGACGCATGGGCGCTGGTTT 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 AATTCACTGCGCCCCAGTCCCTCTTTCCTCCACTTCCTGCTGACGCATGGGCGCTGGTTT 423

Qy        427 TGGGAATTCATCAATGCCACCTTCATCCGTGACATGCTCATGCGTCTGGTACTCACAGCG 486
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Db        424 TGGGAATTCATCAATGCCACCTTCATCCGTGACATGCTCATGCGTCTGGTACTCACAGCG 483

Qy        487 CGTTCCAACCTTATCCCCAGTCCTCCCACCTACAACATAGCGCATGACTACATCAGCTGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CGTTCCAACCTTATCCCCAGTCCTCCCACCTACAACATAGCGCATGACTACATCAGCTGG 543

Qy        547 GAGTCCTTCTCCAATGTGAGCTATTACACTCGTGTTCTGCCCTCTGTGCCCCAAGATTGC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GAGTCCTTCTCCAATGTGAGCTATTACACTCGTGTTCTGCCCTCTGTGCCCCAAGATTGC 603

Qy        607 CCCACGCCCATGGGGACCAAAGGGAAGAAGCAGTTGCCAGACGCCCAACTCCTGGGCCGT 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CCCACGCCCATGGGGACCAAAGGGAAGAAGCAGTTGCCAGACGCCCAACTCCTGGGCCGT 663

Qy        667 CGCTTCCTGCTCAGGAGGAAGTTCATACCTGACCCCCAAGGCACCAACCTCATGTTCGCC 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CGCTTCCTGCTCAGGAGGAAGTTCATACCTGACCCCCAAGGCACCAACCTCATGTTCGCC 723

Qy        727 TTCTTTGCACAACACTTCACCCATCAGTTCTTCAAAACTTCTGGCAAGATGGGTCCTGGC 786
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Db        724 TTCTTTGCACAACACTTCACCCATCAGTTCTTCAAAACTTCTGGCAAGATGGGTCCTGGC 783

Qy        787 TTCACCAAGGCCTTGGGCCATGGGGTAGATCTTGGCCACATTTATGGGGACAATCTGGAC 846
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Db        784 TTCACCAAGGCCTTGGGCCATGGGGTAGATCTTGGCCACATTTATGGGGACAATCTGGAC 843

Qy        847 CGTCAGTATCAGCTGCGGCTCTTTAAGGATGGGAAACTCAAGTATCAGGTTCTGGATGGA 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CGTCAGTATCAGCTGCGGCTCTTTAAGGATGGGAAACTCAAGTATCAGGTTCTGGATGGA 903

Qy        907 GAGATGTACCCGCCATCTGTGGAGGAGGCGCCTGTGTTGATGCACTACCCACGGGGCATT 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GAGATGTACCCGCCATCTGTGGAGGAGGCGCCTGTGTTGATGCACTACCCACGGGGCATT 963

Qy        967 CTGCCCCAGAGTCAGATGGCCGTGGGCCAGGAGGTGTTTGGGCTGCTTCCTGGGCTCATG 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 CTGCCCCAGAGTCAGATGGCCGTGGGCCAGGAGGTGTTTGGGCTGCTTCCTGGGCTCATG 1023
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Qy       1027 CTCTATGCCACGCTCTGGCTGCGTGAGCACAATCGTGTGTGTGACCTGCTGAAGGCTGAG 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 CTCTATGCCACGCTCTGGCTGCGTGAGCACAATCGTGTGTGTGACCTGCTGAAGGCTGAG 1083

Qy       1087 CACCCCACTTGGGGTGATGAGCAACTCTTCCAGACGGCCCGACTCATCCTCATTGGGGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 CACCCCACTTGGGGTGATGAGCAACTCTTCCAGACGGCCCGACTCATCCTCATTGGGGAG 1143

Qy       1147 ACCATCAAGATTGTGATTGAGGAGTATGTGCAGCAGCTGAGTGGCTACTTCTTGCAGCTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 ACCATCAAGATTGTGATTGAGGAGTATGTGCAGCAGCTGAGTGGCTACTTCTTGCAGCTG 1203

Qy       1207 AAGTTCGACCCGGAGCTGCTGTTTAGCGCCCAGTTCCAGTACCGCAACCGCATCGCCATG 1266
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Db       1204 AAGTTCGACCCGGAGCTGCTGTTTAGCGCCCAGTTCCAGTACCGCAACCGCATCGCCATG 1263

Qy       1267 GAGTTCAACCAGCTGTACCACTGGCACCCGCTCATGCCAGACTCCTTCTGGGTGGGTTCC 1326
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Db       1264 GAGTTCAACCAGCTGTACCACTGGCACCCGCTCATGCCAGACTCCTTCTGGGTGGGTTCC 1323

Qy       1327 CAGGAGTACAGCTATGAGCAGTTCCTGTTCAACACCTCCATGCTGACGCACTACGGGATC 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 CAGGAGTACAGCTATGAGCAGTTCCTGTTCAACACCTCCATGCTGACGCACTACGGGATC 1383

Qy       1387 GAGGCCCTGGTGGATGCCTTCTCTCGCCAGAGCGCCGGCCGGATTGGTGGAGGTAGAAAC 1446
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Db       1384 GAGGCCCTGGTGGATGCCTTCTCTCGCCAGAGCGCCGGCCGGATTGGTGGAGGTAGAAAC 1443

Qy       1447 ATAGACCACCATGTCCTGCACGTGGCTGTGGAAACCATCAAGGAATCCCGCGAGTTGCGG 1506
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Qy       1507 CTGCAGCCCTTCAATGAGTACCGCAAGAGGTTTGGCATGAGGCCCTACATGTCCTTCCAG 1566
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Qy       1627 GCCTTGGAATTCTACCCGGGGCTTCTTCTGGAGAAGTGCCATCCAAACTCCATCTTTGGA 1686
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Qy       1687 GAGAGTATGATAGAAATTGGGGCTCCCTTCTCCCTTAAGGGCCTCCTAGGGAATCCCATC 1746
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Db       1864 TTCCGTGTGCCTGACCCCCACCAGGATGGCGGGCCTGGTGTGCAGCGGCCGTCCACAGAG 1923

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Db         1924 CTCTGAGGGGGCAGAGCAGCAGCATTCTGGAGGGTGGACTTGTCATCCCAGAATGCTGAG 1983

Qy         1987 GCTGGGGTTAATAATCCCAAATGTTGGGTCTTTGGTTTGCCTCAAGAATATCAAGGTCAA 2046
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Qy         2047 CATTTAGAACTTTGTGTCTCTCACCCATTATCTGGAATATCATGGTCTTGTTTGTTATTC 2106
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Db         2044 CATTTAGAACTTTGTGTCTCTCACCCATTATCTGGAATATCATGGTCTTGTTTGTTATTC 2103

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Qy         2227 TAGGCATTCTCTAATGTGAAGCTCCTGACAGAATCATCTAGAAAGATAGGGGATTCTTAT 2286
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Db         2224 TAGGCATTCTCTAATGTGAAGCTCCTGACAGAATCATCTAGAAAGATAGGGGATTCTTAT 2283

Qy         2287 TTTGCATTCTAGAATTCTGGGCAGCCCTCCAGCATGTTGATTTTTTTCACTGGCAGTTCA 2346
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Qy         2347 GAATGTTGTGCTCTTGATTGCTGATCCAAAATAGTGGCTGGTATGCCAGATCAGTCTTGC 2406
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Qy         2527 AGGGGGCAGAGTGTTCTTCCTGGGATGCTGACTCAGACCCTGGTCCAAGGAGATAGAACA 2586
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Qy         2587 GGTGGGCTTTTTCCAGGTCATTGGTTGGAGGCCACCAGAGCTCTGTTGCCATCTTTGTCT 2646
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Qy         2647 TGACTCATGACAGCTGTTTCTCATGAAACTAATAAAATTTTTTTTCC 2693
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Database :       N_Geneseq_8:*
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                15:  geneseqn2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                %
Result          Query
   No.   Score  Match Length DB  ID                      Description
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c   1     2693  100.0   2693  6  ABK88561 own            Abk88561 Dog prost
    2     2693  100.0   2693  6  ABK88560 own            Abk88560 DNA encod
    3     2693  100.0   2693 12   ADO52595                Ado52595 Dog COX-1
c   4     2693  100.0   2693 12   ADO52597                Ado52597 Dog COX-1
    5   2677.4   99.4   2706 10   ADD27917 bad date       Add27917 Human COX
    6   2561.2   95.1   2587  6  ABA94341                Aba94341 Canine cy
    7     1899   70.5   1899  6  ABK88562                Abk88562 Dog prost
c   8     1899   70.5   1899  6  ABK88563                Abk88563 Dog prost
c   9     1899   70.5   1899 12   ADO52599                Ado52599 Dog COX-1
   10     1899   70.5   1899 12   ADO52598                Ado52598 Dog COX-1
   11   1898.8   70.5   1902 10   ADD27915                Add27915 Human COX
   12   1808.4   67.2   5049  8  ABX63327                Abx63327 Human
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RESULT 6
ABA94341
ID   ABA94341 standard; DNA; 2587 BP.
XX
AC   ABA94341;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Canine cyclooxygenase-1 (COX-1) protein encoding DNA.
XX
KW   Cyclooxygenase; COX-1; COX-2; canine; arthritis; cancer; neoplasia;
KW   inflammation; central nervous system; dog; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             14. .1825
FT                   /*tag=  a
FT                   /product= "COX-1"
FT                   /note= "the corresponding protein (ABB07241) has few
FT                   unknown residues Xaa for which the encoding codons are
FT                   not indicated in this DNA sequence"
XX
PN   WO200111026-A1.
XX
PD   15-FEB-2001.
XX
PF   04-AUG-2000; 2000WO-US019565.
XX
PR   06-AUG-1999;   99US-0147601P.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Gierse JK;
XX
DR   WPI; 2002-113777/15.
DR   P-PSDB; ABB07241.
XX
PT   Novel substantially purified canine cyclooxygenase 1 or 2 protein, useful
PT   for identifying drugs that can reduce inflammation in dogs, and screening
PT   selective inhibitors of cyclooxygenase-2 protein.
XX
PS   Claim 1; Page 79-81; 122pp; English.
XX
CC   The invention relates to genes that encode canine cyclooxygenase (COX)-1
CC   or COX-2 proteins. The COX proteins, especially COX-2 is useful for
CC   diagnosing or prognosing a COX-2 related condition in a dog. COX-2 or its
CC   fragment is useful for identifying a test material which has the ability
CC   to inhibit, suppress, modulate, or maintain canine COX-2 activity. The
CC   COX-1 and COX-2 polynucleotides are useful for determining an association
CC   between a polymorphism and a trait. COX-2 cDNA molecules and methods
CC   provided are also useful for diagnosing or prognosing COX-2 related
CC   condition such as arthritis, cancer, neoplasia, inflammation or central
CC   nervous system disorder in a dog. The present sequence represents a
CC   canine COX-1 protein encoding DNA
XX
SQ   Sequence 2587 BP; 542 A; 718 C; 681 G; 646 T; 0 U; 0 Other;

  Query Match             95.1%;  Score 2561.2;  DB 6;  Length 2587;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2563;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy        128 GGGGGAGTCGCCTGCACCGGTGGCCGCTGCTCCTGCTGCTGCTGCTGCTGCTGCCGCCGC 187
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Db         21 GGGGGAGTCGCCTGCACCGGTGGCCGCTGCTCCTGCTGCTGCTGCTGCTGCTCCCGCCGC 80

Qy        188 CCCCGGTCCTGCCCGCGGAAGCCCGGACCCCGGCGCCTGTGAACCCGTGTTGTTACTACC 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CCCCGGTCCTGCCCGCGGAAGCCCGGACCCCGGCGCCTGTGAACCCGTGTTGTTACTACC 140

Qy        248 CATGTCAGCACCAAGGGATCTGTGTCCGCTTCGGCCTTGACCGCTACCAGTGTGACTGCA 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 CATGTCAGCACCAAGGGATCTGTGTCCGCTTCGGCCTTGACCGCTACCAGTGTGACTGCA 200

Qy        308 CCCGCACGGGCTATTCTGGCCCCAACTGCACCATCCCCGAGCTGTGGACCTGGCTCCGGA 367
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Db        201 CCCGCACGGGCTATTCTGGCCCCAACTGCACCATCCCCGAGCTGTGGACCTGGCTCCGGA 260

Qy        368 ATTCACTGCGCCCCAGTCCCTCTTTCCTCCACTTCCTGCTGACGCATGGGCGCTGGTTTT 427
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Qy        428 GGGAATTCATCAATGCCACCTTCATCCGTGACATGCTCATGCGTCTGGTACTCACAGCGC 487
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Qy        488 GTTCCAACCTTATCCCCAGTCCTCCCACCTACAACATAGCGCATGACTACATCAGCTGGG 547
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Db        381 GTTCCAACCTTATCCCCAGTCCTCCCACCTACAACATAGCGCATGACTACATCAGCTGGG 440

Qy        548 AGTCCTTCTCCAATGTGAGCTATTACACTCGTGTTCTGCCCTCTGTGCCCCAAGATTGCC 607
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Qy        608 CCACGCCCATGGGGACCAAAGGGAAGAAGCAGTTGCCAGACGCCCAACTCCTGGGCCGTC 667
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Db        501 CCACGCCCATGGGGACCAAAGGGAAGAAGCAGTTGCCAGACGCCCAACTCCTGGGCCGTC 560

Qy        668 GCTTCCTGCTCAGGAGGAAGTTCATACCTGACCCCCAAGGCACCAACCTCATGTTCGCCT 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 GCTTCCTGCTCAGGAGGAAGTTCATACCTGACCCCCAAGGCACCAACCTCATGTTCGCCT 620

Qy        728 TCTTTGCACAACACTTCACCCATCAGTTCTTCAAAACTTCTGGCAAGATGGGTCCTGGCT 787
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Db        621 TCTTTGCACAACACTTCACCCATCAGTTCTTCAAAACTTCTGGCAAGATGGGTCCTGGCT 680

Qy        788 TCACCAAGGCCTTGGGCCATGGGGTAGATCTTGGCCACATTTATGGGGACAATCTGGACC 847
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Db        681 TCACCAAGGCCTTGGGCCATGGGGTAGATCTTGGCCACATTTATGGGGACAATCTGGACC 740

Qy        848 GTCAGTATCAGCTGCGGCTCTTTAAGGATGGGAAACTCAAGTATCAGGTTCTGGATGGAG 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GTCAGTATCAGCTGCGGCTCTTTAAGGATGGGAAACTCAAGTATCAGGTTCTGGATGGAG 800

Qy        908 AGATGTACCCGCCATCTGTGGAGGAGGCGCCTGTGTTGATGCACTACCCACGGGGCATTC 967
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Db        801 AGATGTACCCGCCATCTGTGGAGGAGGCGCCTGTGTTGATGCACTACCCACGGGGCATTC 860

Qy        968 TGCCCCAGAGTCAGATGGCCGTGGGCCAGGAGGTGTTTGGGCTGCTTCCTGGGCTCATGC 1027
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Db        861 TGCCCCAGAGTCAGATGGCCGTGGGCCAAGAAGTGTTTGGGCTGCTTCCTGGGCTCATGC 920
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Qy       1028 TCTATGCCACGCTCTGGCTGCGTGAGCACAATCGTGTGTGTGACCTGCTGAAGGCTGAGC 1087
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Qy       1148 CCATCAAGATTGTGATTGAGGAGTATGTGCAGCAGCTGAGTGGCTACTTCTTGCAGCTGA 1207
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Qy       1208 AGTTCGACCCGGAGCTGCTGTTTAGCGCCCAGTTCCAGTACCGCAACCGCATCGCCATGG 1267
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Qy       1328 AGGAGTACAGCTATGAGCAGTTCCTGTTCAACACCTCCATGCTGACGCACTACGGGATCG 1387
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Qy       1568 AACTCACAGGGGAGAAGGAGATGGCAGCCGAGTTGGAGGAGCTGTATGGAGACATTGATG 1627
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Qy       1868 TCCGTGTGCCTGACCCCCACCAGGATGGCGGGCCTGGTGTGGAGCGGCCGTCCACAGAGC 1927
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Qy       1928 TCTGAGGGGGCAGAGCAGCAGCATTCTGGAGGGTGGACTTGTCATCCCAGAATGCTGAGG 1987
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Db       1821 TCTGAGGGGGCAGAGCAGCAGCATTCTGGAGGGTGGACTTGTCATCCCAGAATGCTGAGG 1880

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Db       1881 CTGGGGTTAATAATCCCAAATGTTGGGTCTTTGGTTTGCCTCAAGAATATCAAGGTCAAC 1940

Qy       2048 ATTTAGAACTTTGTGTCTCTCACCCATTATCTGGAATATCATGGTCTTGTTTGTTATTCT 2107
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Qy       2108 AGAATGCTGAATTCCTGGTTGACCATCTAGAATGGATGGAGTGATGCTTCTTTGGCAAGC 2167
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Db       2001 AGAATGCTGAATTCCTGGTTGACCATCTAGAATGGATGGAGTGATGCTTCTTTGGCAAGC 2060

Qy       2168 CAGAACACTGGTTCCTGGCCGACAACCTAGAATGTCAGACTTCTGGTTGACTTAAGACGT 2227
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Qy       2228 AGGCATTCTCTAATGTGAAGCTCCTGACAGAATCATCTAGAAAGATAGGGGATTCTTATT 2287
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Qy       2288 TTGCATTCTAGAATTCTGGGCAGCCCTCCAGCATGTTGATTTTTTTCACTGGCAGTTCAG 2347
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Qy       2348 AATGTTGTGCTCTTGATTGCTGATCCAAAATAGTGGCTGGTATGCCAGATCAGTCTTGCT 2407
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Qy       2408 CTGAATGCCTAGAATGGTAATTTGATTCATTTTCCTGTTCAGTGAGATACCCCCAAAGCA 2467
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Qy       2468 GGAGAATCTACAGCCTAACCAGAGTGCATTGCCTGCCTCTGTGCCTGCCCCAAGGACTTA 2527
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Db       2361 GGAGAATCTACAGCCTAACCAGAGTGCATTGCCTGCCTCTGTGCCTGCCCCAAGGACTTA 2420

Qy       2528 GGGGGCAGAGTGTTCTTCCTGGGATGCTGACTCAGACCCTGGTCCAAGGAGATAGAACAG 2587
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Db       2421 GGGGGCAGAGTGTTCTTCCTGGGATGCTGACTCAGACCCTGGTCCAAGGAGATAGAACAG 2480

Qy       2588 GTGGGCTTTTTCCAGGTCATTGGTTGGAGGCCACCAGAGCTCTGTTGCCATCTTTGTCTT 2647
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Db       2481 GTGGGCTTTTTCCAGGTCATTGGTTGGAGGCCACCAGAGCTCTGTTGCCATCTTTGTCTT 2540

Qy       2648 GACTCATGACAGCTGTTTCTCATGAAACTAATAAAATTTTTTTTCC 2693
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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     4   703.6   26.1   3356  7  US-11-242-111-2              Sequence 2, Appli
     5      42    1.6   1661  6  US-10-196-749-229            Sequence 229, App
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     7      41    1.5   1167  7  US-11-113-081A-9             Sequence 9, Appli
     8    39.8    1.5   1788  6  US-10-196-749-405            Sequence 405, App
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c   11      39    1.4    790  7  US-11-301-554-1865           Sequence 1865, Ap
c   12      39    1.4   1635  7  US-11-301-554-1798           Sequence 1798, Ap
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    Pred. No. is the number of results predicted by chance to have a
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                                   SUMMARIES
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Result         Query
   No.  Score  Match Length DB ID                           Description
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     3   2693  100.0   2693  8 US-10-679-140-12              Sequence 12, Appl
c    4   2693  100.0   2693  8 US-10-679-140-14              Sequence 14, Appl
     5 2677.4   99.4   2706  7 US-10-260-937-3  ]            Sequence 3, Appli
     6 2630.6   97.7   2682  7 US-10-260-937-57 ]            Sequence 57, Appl
     7 2561.2   95.1   2587  7 US-10-260-937-55              Sequence 55, Appl
     8   1899   70.5   1899  3 US-09-919-060-15              Sequence 15, Appl
c    9   1899   70.5   1899  3 US-09-919-060-16              Sequence 16, Appl
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c   11   1899   70.5   1899  8 US-10-679-140-16              Sequence 16, Appl
    12 1898.8   70.5   1902  7 US-10-260-937-1               Sequence 1, Appli
    13 1808.4   67.2   5049  3 US-09-971-392-167             Sequence 167, App
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      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                        SUMMARIES
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Result           Query
   No.    Score  Match Length DB  ID                           Description
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 c    2    2693  100.0   2693  3  US-09-919-060-14              Sequence 14, Appl
      3    1899   70.5   1899  3  US-09-919-060-15              Sequence 15, Appl
 c    4    1899   70.5   1899  3  US-09-919-060-16              Sequence 16, Appl
      5  1803.8   67.0   2539  3  US-09-949-016-3943            Sequence 3943, Ap
      6  1794.2   66.6   2554  3  US-09-949-016-137             Sequence 137, App
      7  1771.2   65.8   2554  2  US-08-627-254C-28             Sequence 28, Appl
      8  1483.4   55.1   1819  2  US-08-487-753-6               Sequence 6, Appli
      9  1483.4   55.1   1819  2  US-08-480-065-6               Sequence 6, Appli
     10  1483.4   55.1   1819  3  US-08-487-744-6               Sequence 6, Appli
     11  1483.4   55.1   1819  7  PCT-US93-09167-6              Sequence 6, Appli
     12  1476.6   54.8   1920  3  US-08-459-493-2               Sequence 2, Appli
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                             SUMMARIES
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Result                  Query
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     4    1332.6        49.5    2353  6  AK142741                    AK142741 Mus muscu
     5    1332.6        49.5    2355  6  AK163609                    AK163609 Mus muscu
     6    1332.6        49.5    2793  6  AK046457                    AK046457 Mus muscu
     7    1332.6        49.5    2865  6  AK159907                    AK159907 Mus muscu
     8      1331        49.4    2323  6  AK170414                    AK170414 Mus muscu
     9      1328        49.3    2003  6  AK170664                    AK170664 Mus muscu
    10    1306.2        48.5    2788  6  AK160886                    AK160886 Mus muscu
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     3    626   98.9    634  7  ADD27916                     Add27916 Human COX
     4    574   90.7    608  5  ABB07241                     Abb07241 Canine cy
     5    499   78.8    603  7  ADD27938                     Add27938 Canine CO
     6    256   40.4    415  7  ADD27919                     Add27919 Human PCO
     7     87   13.7    600  7  ADD27937                     Add27937 Ovine COX
     8     71   11.2    440  9  ADZ59939                     Adz59939 Human COX
     9     71   11.2    489  9  ADW72143                     Adw72143 Human COX
    10     71   11.2    514  7  ADD12559                     Add12559 Human ENZ
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      and is derived by analysis of the total score distribution.

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     4  2042.5    59.3    604  2  US-09-919-060-5             Sequence 5, Appli
     5  2029.5    58.9    604  1  US-08-064-271-10            Sequence 10, Appl
     6  2029.5    58.9    604  1  US-08-487-753-4             Sequence 4, Appli
     7  2029.5    58.9    604  1  US-08-480-065-4             Sequence 4, Appli
     8  2029.5    58.9    604  2  US-08-487-744-4             Sequence 4, Appli
     9  2029.5    58.9    604  2  US-08-930-589A-18           Sequence 18, Appl
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; Sequence 9814, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9814
;   LENGTH: 596
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9814

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Qy        104 IPELWTWLRNSLRPSPSFLHFLLTHGRWFWEFINATFIRDMLMRLVLTARSNLIPSPPTY 163
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Qy        164 NIAHDYISWESFSNVSYYTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRRKFIPD 223
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Qy        284 KLKYQVLDGEMYPPSVEEAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLWLREHN 343
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Qy        404 FQYRNRIAMEFNQLYHWHPLMPDSFWVGSQEYSYEQFLFNTSMLTHYGIEALVDAFSRQS 463
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Qy        464 AGRIGGGRNIDHHVLHVAVETIKESRELRLQPFNEYRKRFGMRPYMSFQELTGEKEMAAE 523
              |||||||||:|||:|||||: |:||||:||||||||||||||:|| ||||| ||||||||
Db        427 AGRIGGGRNMDHHILHVAVDVIRESREMRLQPFNEYRKRFGMKPYTSFQELVGEKEMAAE 486
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Qy        524 LEELYGDIDALEFYPGLLLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYWKPSTF 583
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Qy        584 GGEMGFNMVKTATLKKLVCLNTKTCPYVSFRVPDPHQDGGPGVERPSTEL 633
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      Pred. No. is the number of results predicted by chance to have a
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      and is derived by analysis of the total score distribution.

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     3    3440    99.9    633  4  US-10-260-937-2              Sequence 2, Appli
     4  3427.5    99.5    632  4  US-10-260-937-60             Sequence 60, Appl
     5    3261    94.7    603  4  US-10-260-937-58             Sequence 58, Appl
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; Sequence 2, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Daniel
;  APPLICANT:  Chandrasekharan, N. Vishvanath
;  TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 07913-007001
;  CURRENT APPLICATION NUMBER: US/10/260,937
;  CURRENT FILING DATE:  2002-09-28
;  PRIOR APPLICATION NUMBER: US 60/326,133
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US 60/373,225
;  PRIOR FILING DATE: 2002-04-15
;  PRIOR APPLICATION NUMBER: US 60/373,661
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: US 60/411,575
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 633
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-10-260-937-2

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Db        121 FLHFLLTHGRWFWEFINATFIRDMLMRLVLTARSNLIPSPPTYNIAHDYISWESFSNVSY 180

Qy        181 YTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRRKFIPDPQGTNLMFAFFAQHFTH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 YTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRRKFIPDPQGTNLMFAFFAQHFTH 240

Qy        241 QFFKTSGKMGPGFTKALGHGVDLGHIYGDNLDRQYQLRLFKDGKLKYQVLDGEMYPPSVE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QFFKTSGKMGPGFTKALGHGVDLGHIYGDNLDRQYQLRLFKDGKLKYQVLDGEMYPPSVE 300

Qy        301 EAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLWLREHNRVCDLLKAEHPTWGDEQ 360
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Db        301 EAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLWLREHNRVCDLLKAEHPTWGDEQ 360

Qy        361 LFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFSAQFQYRNRIAMEFNQLYHW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFSAQFQYRNRIAMEFNQLYHW 420

Qy        421 HPLMPDSFWVGSQEYSYEQFLFNTSMLTHYGIEALVDAFSRQSAGRIGGGRNIDHHVLHV 480
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Db        421 HPLMPDSFWVGSQEYSYEQFLFNTSMLTHYGIEALVDAFSRQSAGRIGGGRNIDHHVLHV 480

Qy        481 AVETIKESRELRLQPFNEYRKRFGMRPYMSFQELTGEKEMAAELEELYGDIDALEFYPGL 540
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Db        481 AVETIKESRELRLQPFNEYRKRFGMRPYMSFQELTGEKEMAAELEELYGDIDALEFYPGL 540

Qy        541 LLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYWKPSTFGGEMGFNMVKTATLKKL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYWKPSTFGGEMGFNMVKTATLKKL 600

Qy        601 VCLNTKTCPYVSFRVPDPHQDGGPGVERPSTEL 633
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
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Result             Query
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     4     2799    81.3     602  2  A35564                   prostaglandin-endo
     5   2794.5    81.2     600  2  A28960                   prostaglandin-endo
     6     2791    81.1     602  2  S69198                   prostaglandin G/H
     7     2745    79.7     602  2  S39782                   cyclooxygenase 1 -
     8   2070.5    60.1     603  2  A38630                   prostaglandin-endo
     9   2032.5    59.0     603  2  JC5063                   prostaglandin-endo
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    11   2024.5    58.8     604  2  A49010                   prostaglandin-endo
    12   2011.5    58.4     604  2  JC2030                   prostaglandin-endo
    13      261     7.6     643  2  T03631                   oxygenase, pathoge
    14    255.5     7.4     631  2  H96763                   feebly-like protei
    15    254.5     7.4    1475  2  T29809                   hypothetical prote
    16      254     7.4    1506  2  T32909                   hypothetical prote
    17      219     6.4    1313  2  T29027                   hypothetical prote
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                           SUMMARIES
                     %
Result               Query
   No.    Score      Match Length DB  ID                          Description
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     1     3440      99.9    633  2  Q8HZR1_CANFA                Q8hzr1 canis famil
     2   3010.5      87.4    630  2  Q3HY28_HUMAN                Q3hy28 homo sapien
     3   3004.5      87.3    630  2  Q3HY29_HUMAN                Q3hy29 homo sapien
     4     2991      86.9    599  1  PGH1_HUMAN                  P23219 homo sapien
     5     2991      86.9    599  2  Q5T7T7_HUMAN                Q5t7t7 homo sapien
     6   2954.5      85.8    600  1  PGH1_SHEEP                  P05979 ovis aries
     7     2915      84.7    606  1  PGH1_RABIT                  O97554 oryctolagus
     8   2807.5      81.5    617  2  Q8CIL6_MOUSE                Q8cil6 mus musculu
     9     2802      81.4    602  2  Q3UZ23_MOUSE                Q3uz23 mus musculu
    10   2800.5      81.3    562  2  Q5T7T8_HUMAN                Q5t7t8 homo sapien
    11     2799      81.3    602  1  PGH1_MOUSE                  P22437 mus musculu
    12     2799      81.3    602  2  Q543T1_MOUSE                Q543t1 m adult mal
    13     2792      81.1    602  2  Q66HK3_RAT                  Q66hk3 rattus norv
    14     2791      81.1    602  1  PGH1_RAT                    Q63921 rattus norv
    15     2296      66.7    488  2  Q3TJN9_MOUSE                Q3tjn9 mus musculu
    16     2280      66.2    598  2  Q9PTN3_SALFO                Q9ptn3 salvelinus
    17   2260.5      65.7    624  2  Q9DEQ0_ONCMY                Q9deq0 oncorhynchu
    18   2252.5      65.4    597  2  Q8JH44_BRARE                Q8jh44 brachydanio
    19     2223      64.6    589  2  Q4SUV4_TETNG                Q4suv4 tetraodon n
    20   2147.5      62.4    593  2  Q8UVQ3_SQUAC                Q8uvq3 squalus aca
    21   2138.5      62.1    414  2  Q8HZR0_CANFA                Q8hzr0 canis famil
    22   2070.5      60.1    603  1  PGH2_CHICK                  P27607 gallus gall
```

```
RESULT 1
Q8HZR1_CANFA
ID   Q8HZR1_CANFA   PRELIMINARY;   PRT;   633 AA.
AC   Q8HZR1;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-MAR-2006, entry version 19.
DE   Cyclooxygenase.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22269907; PubMed=12242329; DOI=10.1073/pnas.162468699;
RA   Chandrasekharan N.V., Dai H., Roos K.L.T., Evanson N.K., Tomsik J.,
RA   Elton T.S., Simmons D.L.;
RT   "COX-3, a cyclooxygenase-1 variant inhibited by acetaminophen and
RT   other analgesic/antipyretic drugs: cloning, structure, and
RT   expression.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:13926-13931(2002).
CC   -!- FUNCTION: May have a role as a major mediator of inflammation
CC       and/or a role for prostanoid signaling in activity-dependent
CC       plasticity (By similarity).
CC   -!- CATALYTIC ACTIVITY: Arachidonate + AH(2) + 2 O(2) = prostaglandin
CC       H(2) + A + H(2)O.
CC   -!- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
CC       molecule (By similarity).
CC   -!- PATHWAY: Fatty acids biosynthesis; prostaglandin biosynthesis.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane-associated. Microsomal membrane (By
CC       similarity).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AF535138; AAN33049.1; -; mRNA.
DR   HSSP; P05979; 1Q4G.
DR   SMR; Q8HZR1; 65-617.
DR   Ensembl; ENSCAFG00000020263; Canis familiaris.
DR   GO; GO:0004601; F:peroxidase activity; IEA.
DR   InterPro; IPR002007; Anim_peroxidase.
DR   InterPro; IPR000742; EGF_3.
DR   InterPro; IPR006209; EGF_like.
DR   Pfam; PF03098; An_peroxidase; 2.
DR   Pfam; PF00008; EGF; 1.
DR   PRINTS; PR00457; ANPEROXIDASE.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS50292; PEROXIDASE_3; 1.
KW   Dioxygenase; Fatty acid biosynthesis; Heme; Iron; Lipid synthesis;
KW   Metal-binding; Oxidoreductase; Peroxidase; Prostaglandin biosynthesis.
SQ   SEQUENCE   633 AA;  72503 MW;  D338221B976BDB7E CRC64;

  Query Match             99.9%;  Score 3440;  DB 2;  Length 633;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-259;
  Matches  632;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSREFDPEAPRNPLRLPGEPRMPGPALTSRSAGGSRLHRWPLLLLLLLLLPPPPVLPAEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSREFDPEAPRNPLRLPGEPRMPGPALTSRSAGGSRLHRWPLLLLLLLLLPPPPVLPAEA 60
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Qy         61 RTPAPVNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYSGPNCTIPELWTWLRNSLRPSPS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RTPAPVNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYSGPNCTIPELWTWLRNSLRPSPS 120

Qy        121 FLHFLLTHGRWFWEFINATFIRDMLMRLVLTARSNLIPSPPTYNIAHDYISWESFSNVSY 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FLHFLLTHGRWFWEFINATFIRDMLMRLVLTARSNLIPSPPTYNIAHDYISWESFSNVSY 180

Qy        181 YTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRRKFIPDPQGTNLMFAFFAQHFTH 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 YTRVLPSVPQDCPTPMGTKGKKQLPDAQLLGRRFLLRRKFIPDPQGTNLMFAFFAQHFTH 240

Qy        241 QFFKTSGKMGPGFTKALGHGVDLGHIYGDNLDRQYQLRLFKDGKLKYQVLDGEMYPPSVE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QFFKTSGKMGPGFTKALGHGVDLGHIYGDNLDRQYQLRLFKDGKLKYQVLDGEMYPPSVE 300

Qy        301 EAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLWLREHNRVCDLLKAEHPTWGDEQ 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EAPVLMHYPRGILPQSQMAVGQEVFGLLPGLMLYATLWLREHNRVCDLLKAEHPTWGDEQ 360

Qy        361 LFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFSAQFQYRNRIAMEFNQLYHW 420
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Db        361 LFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFSAQFQYRNRIAMEFNQLYHW 420

Qy        421 HPLMPDSFWVGSQEYSYEQFLFNTSMLTHYGIEALVDAFSRQSAGRIGGGRNIDHHVLHV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 AVETIKESRELRLQPFNEYRKRFGMRPYMSFQELTGEKEMAAELEELYGDIDALEFYPGL 540

Qy        541 LLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYWKPSTFGGEMGFNMVKTATLKKL 600
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Db        541 LLEKCHPNSIFGESMIEIGAPFSLKGLLGNPICSPEYWKPSTFGGEMGFNMVKTATLKKL 600

Qy        601 VCLNTKTCPYVSFRVPDPHQDGGPGVERPSTEL 633
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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 c   4   268.6   97.7   1899  2   AR411938                  AR411938 Sequence
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     7   268.6   97.7   2706  14   AF535138                  AF535138 Canis fam
     8   265.4   96.5   2587  2   AX082872                  AX082872 Sequence
     9   244.6   88.9   1793  2   CQ724617                  CQ724617 Sequence
    10   244.6   88.9   1797  2   E03346                    E03346 DNA sequenc
    11   244.6   88.9   1800  8   AY892997                  AY892997 Synthetic
    12   244.6   88.9   1812  5   S78220                    S78220 prostagland
    13   244.6   88.9   1819  2   AR055230                  AR055230 Sequence
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    15   244.6   88.9   1893  2   CQ869572                  CQ869572 Sequence
    16   244.6   88.9   1893  5   DQ180741                  DQ180741 Homo sapi
    17   244.6   88.9   1893  5   DQ180742                  DQ180742 Homo sapi
    18   244.6   88.9   2324  5   S36219                    S36219 prostagland
    19   244.6   88.9   2435  5   S36271                    S36271 prostagland
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                              GenCore version 5.1.9
                   Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  8, 2006, 04:28:49 ; Search time 37.4947 Seconds
                                           (without alignments)
                                           13723.414 Million cell updates/sec

Title:          US-10-679-140-9
Perfect score:  275
Sequence:       1 tttgcacaacacttcaccca..........gctgtgggccaggaggtgtt 275

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
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     3   268.6   97.7   1899  3  US-09-919-060-15             Sequence 15, Appl
 c   4   268.6   97.7   1899  3  US-09-919-060-16             Sequence 16, Appl
     5   268.6   97.7   2693  3  US-09-919-060-12             Sequence 12, Appl
 c   6   268.6   97.7   2693  3  US-09-919-060-14             Sequence 14, Appl
     7   244.6   88.9   1819  2  US-08-487-753-6              Sequence 6, Appli
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     9   244.6   88.9   1819  3  US-08-487-744-6              Sequence 6, Appli
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    11   244.6   88.9   2539  3  US-09-949-016-3943           Sequence 3943, Ap
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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                %
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    3    244.6   88.9   1024  1  AL556508                    AL556508 AL556508
    4    244.6   88.9   1473  14  AY415140                    AY415140 Homo sapi
    5    244.6   88.9   1766  4  CD014048                    CD014048 90138112
    6    244.6   88.9   1770  4  CD014049                    CD014049 90138252
    7    244.6   88.9   2132  4  CD014050                    CD014050 90138391
    8      242   88.0   1448  14  AY415141                    AY415141 Pan trogl
    9    233.6   84.9    551  1  AU279462                    AU279462 AU279462
   10    230.2   83.7    702  5  CK963432                    CK963432 4077776 B
   11    214.2   77.9   1448  14  AY415142                    AY415142 Mus muscu
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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                                 SUMMARIES
                    %
Result              Query
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 c   2      275     100.0     275   3  US-09-919-060-11                   Sequence 11, Appl
     3      275     100.0     275   8  US-10-679-140-9                    Sequence 9, Appli
 c   4      275     100.0     275   8  US-10-679-140-11                   Sequence 11, Appl
     5    268.6      97.7    1899   3  US-09-919-060-15                   Sequence 15, Appl
 c   6    268.6      97.7    1899   3  US-09-919-060-16                   Sequence 16, Appl
     7    268.6      97.7    1899   8  US-10-679-140-15                   Sequence 15, Appl
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    15    265.4      96.5    2587   7  US-10-260-937-55                   Sequence 55, Appl
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
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                 %
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     5   1895.8   99.8   2706 14   AF535138                  AF535138 Canis fam
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    12   1479.4   77.9   1812  5  S78220                    S78220 prostagland
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     9  1476.2   77.7   1819  3  US-08-487-744-6            Sequence 6, Appli
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     5    1311   69.0   2323  6  AK170414                   AK170414 Mus muscu
     6    1311   69.0   2353  6  AK142741                   AK142741 Mus muscu
     7    1311   69.0   2355  6  AK163609                   AK163609 Mus muscu
     8    1311   69.0   2793  6  AK046457                   AK046457 Mus muscu
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    14  1207.6   63.6   1770  4  CD014049                   CD014049 90138252
    15  1203.2   63.4   1766  4  CD014048                   CD014048 90138112
    16    1084   57.1   1448  14  AY415142                   AY415142 Mus muscu
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    19   716.4   37.7   2247  6  AK049923                   AK049923 Mus muscu
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SCORE Search Results Details for Application 10679140 and Search Result us-10-679-140-16.rge.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10679140 and Search Result us-10-679-140-16.rge.

start

Go Back to previous page

```
                        GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July  7, 2006, 15:02:13 ; Search time 7478.95 Seconds
                                           (without alignments)
                                           16237.064 Million cell updates/sec

Title:          US-10-679-140-16
Perfect score:  1899
Sequence:       1 gagctctgtggacggccgct..........gggtcgaactcacggctcat 1899

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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 c    6  1797.2    94.6   2587   2   AX082872                  AX082872 Sequence
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                              ALIGNMENTS


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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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 c   11  1456.4     76.7    2554  2  US-08-627-254C-28           Sequence 28, Appl
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 c  11    1271    66.9   2742  6  AK167357                    AK167357 Mus muscu
 c  12    1238    65.2   1473  14  AY415140                    AY415140 Homo sapi
 c  13  1210.8    63.8   1448  14  AY415141                    AY415141 Pan trogl
 c  14  1207.6    63.6   1770  4  CD014049                    CD014049 90138252
 c  15  1203.2    63.4   1766  4  CD014048                    CD014048 90138112
 c  16    1084    57.1   1448  14  AY415142                    AY415142 Mus muscu
 c  17   753.6    39.7   1024  1  AL556508                    AL556508 AL556508
 c  18   750.2    39.5    884  10  DV919230                    DV919230 LB02915.C
 c  19   716.4    37.7   2247  6  AK049923                    AK049923 Mus muscu
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      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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 c    7     268.6       97.7    2706  14   AF535138                    AF535138 Canis fam
 c    8     265.4       96.5    2587   2  AX082872                    AX082872 Sequence
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 c   10     244.6       88.9    1797   2  E03346                      E03346 DNA sequenc
 c   11     244.6       88.9    1800   8  AY892997                    AY892997 Synthetic
 c   12     244.6       88.9    1812   5  S78220                      S78220 prostagland
 c   13     244.6       88.9    1819   2  AR055230                    AR055230 Sequence
 c   14     244.6       88.9    1860   2  CQ869574                    CQ869574 Sequence
 c   15     244.6       88.9    1893   2  CQ869572                    CQ869572 Sequence
 c   16     244.6       88.9    1893   5  DQ180741                    DQ180741 Homo sapi
 c   17     244.6       88.9    1893   5  DQ180742                    DQ180742 Homo sapi
 c   18     244.6       88.9    2324   5  S36219                      S36219 prostagland
```

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RESULT 10
E03346/c
LOCUS       E03346                  1797 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence coding for human prostaglandin endoperoxidase.
ACCESSION   E03346
VERSION     E03346.1  GI:2171563
KEYWORDS    JP 1992045786-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1797)
  AUTHORS   Tanabe,T.
  TITLE     HUMAN PROSTAGLANDIN ENDOPEROXIDE SYNTHASE
  JOURNAL   Patent: JP 1992045786-A 1 14-FEB-1992;
            MEIJI MILK PROD CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 1992045786-A/1
            PD   14-FEB-1992
            PF   13-JUN-1990 JP 1990152784
            PI   TANABE TADASHI
            PC   C12N9/02,C12N15/53//A61K37/50;
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: tissue_type=Blood;
            CC   *source: cell_line=EMBLS;
            FH   Key             Location/Qualifiers
            FH
            FT   mat_peptide     1. .1797
            FT                   /note='human prostaglandin endoperoxidase'.
FEATURES             Location/Qualifiers
     source          1. .1797
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             88.9%;  Score 244.6;  DB 2;  Length 1797;
  Best Local Similarity   93.1%;  Pred. No. 1.9e-70;
  Matches  256;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 AACACCTCCTGGCCCACAGCCATCTGACTCTGGGGCAGAATGCCCCGTGGGTAGTGCATC 60
              |||||||||||||||||||||||||| ||||||||| | ||||| || ||||||||||||
Db        872 AACACCTCCTGGCCCACAGCCATCTGGCTCTGGGGCGGGATGCCTCGGGGGTAGTGCATC 813

Qy         61 AACACAGGCGCCTCCTCCACAGATGACGGGTACATCTCTCCATCCAGAACCTGATACTTG 120
              |||||||||||||| || || || | ||||||||| ||||||||||| ||||| ||||||
Db        812 AACACAGGCGCCTCTTCTACCGAGGGCGGGTACATTTCTCCATCCAGCACCTGGTACTTG 753

Qy        121 AGTTTCCCATCCTTAAAGAGCCGCAGCTGATACTGACGGTCCAGATTGTCCCCATAAATG 180
              |||||||||||||||||||||||||| ||||||||||| ||||||||||| |||||||||
Db        752 AGTTTCCCATCCTTAAAGAGCCGCAGTTGATACTGACGCTCCAGATTGTCTCCATAAATG 693

Qy        181 TGACCAAGATCTACCCCATGGCCCAAGGCCTTGGTGAAGCCAGGACCCATCTTGCCAGAA 240
              || || || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 TGGCCGAGGTCTACCCCATGGCCCAAGGCCTTGGTGAAGCCAGGACCCATCTTGCCAGAA 633

Qy        241 GTTTTGAAGAACTGGTGGGTGAAGTGTTGTGCAAA 275
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                 |||||||||||||||||||||||||||||||||||
Db           632 GTTTTGAAGAACTGGTGGGTGAAGTGTTGTGCAAA 598
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